

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 23, 2001, 14:18:50 ; Search time 29.33 seconds
(without alignments)
1758.319 Million cell updates/sec

Title: US-08-883-036a-2
Perfect score: 2327
Sequence: 1 MEORGNAPASGARRKRRHP.....HLLSGKPMYLEGNADSAMS 440

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: SPREMBL_15:*
2: sp_archaea:*
3: sp_bacteria:*
4: sp_fungi:*
5: sp_human:*
6: sp_invertebrate:*
7: sp_mhnc:*
8: sp_mammal:*
9: sp_organelle:*
10: sp_phage:*
11: sp_plant:*
12: sp_rodent:*
13: sp_unclassified:*
14: sp_vertebrate:*
15: sp_virus:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2327	100.0	440	014763	014763 homo sapien
2	2313	99.4	440	015531	015531 homo sapien
3	2151.5	92.5	411	015508	015508 homo sapien
4	2138.5	91.9	411	014720	014720 homo sapien
5	2137.5	91.9	411	015517	015517 homo sapien
6	1061.5	45.6	468	000220	000220 homo sapien
7	869	37.3	386	09UBN6	09UBN6 homo sapien
8	855	36.7	386	09Y604	09Y604 homo sapien
9	588	25.3	381	09OZM4	09OZM4 mus musculu
10	580	24.9	381	09JTL6	09JTL6 mus musculu
11	565	24.3	385	09JUL5	09JUL5 mus musculu
12	488.5	21.0	368	057408	057408 meleagris g
13	474.5	20.4	368	09IAR7	09IAR7 gallus gall
14	467	20.1	299	014798	014798 homo sapien
15	464.5	20.0	368	09PW79	09PW79 gallus gall
16	441	19.0	259	014755	014755 homo sapien
17	217	9.3	426	014865	014865 homo sapien
18	203	8.7	418	000275	000275 homo sapien
19	200.5	8.6	387	09PVD4	09PVD4 xenopus lae

20	199.5	8.6	314	4	014293	014293 homo sapien
21	195	8.4	331	6	09TSN4	09TSN4 macaca fasc
22	191	8.2	380	4	000280	000280 homo sapien
23	179	7.7	327	6	097491	097491 ovls aries
24	175.5	7.5	302	13	09PUS0	09PUS0 salvelinus
25	174	7.5	283	6	09XS28	09XS28 cercopithec
26	172	7.4	439	4	016042	016042 homo sapien
27	170	7.3	348	14	057277	057277 monkeypox v
28	170	7.3	372	4	000279	000279 homo sapien
29	168.5	7.2	263	6	09XS60	09XS60 oryctolagus
30	168.5	7.2	319	6	09TV79	09TV79 oryctolagus
31	168.5	7.2	320	6	09XS29	09XS29 oryctolagus
32	168	7.2	348	14	057108	057108 monkeypox v
33	167.5	7.2	349	14	057291	057291 monkeypox v
34	167.5	7.2	349	14	057117	057117 monkeypox v
35	167.5	7.2	349	14	057102	057102 monkeypox v
36	167.5	7.2	459	11	062327	062327 mus musculu
37	166	7.1	348	14	057103	057103 monkeypox v
38	164.5	7.1	349	14	057099	057099 monkeypox v
39	161.5	6.9	349	14	057100	057100 monkeypox v
40	161.5	6.9	351	14	057117	057117 compox viru
41	161	6.9	417	11	09Z0W1	09Z0W1 mus musculu
42	158.5	6.8	482	11	088734	088734 mus musculu
43	157.5	6.8	401	13	09PRG7	09PRG7 xenopus lae
44	155	6.7	189	6	097530	097530 canis faml
45	154.5	6.6	616	4	09Y606	09Y606 homo sapien

ALIGNMENTS

RESULT	ID	PRELIMINARY	PRT	440 AA.
014763	014763			
AC	014763			
DT	01-JAN-1998 (TREMBLrel. 05, Created)			
DT	01-JAN-1998 (TREMBLrel. 05, Last sequence update)			
DT	01-OCT-2000 (TREMBLrel. 15, Last annotation update)			
DE	APOPTOSIS INDUCING RECEPTOR TRAIL-R2.			
GN	TRAILR2.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_Taxid=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE-97459925; Pubmed-9311998;			
RA	Walczak H., Degli-Esposti M.A., Johnson R.S., Smolak P.J., Waugh J.Y.,			
RA	Bolant M., Timour M.S., Gerhart M.J., Schooley K.A., Smith C.A.,			
RA	Goodwin R.G., Rauch C.T.;			
RT	"TRAIL-R2: a novel apoptosis-mediating receptor for TRAIL.";			
RL	EMBO J. 16:5386-5397(1997).			
DR	EMBL; AF016849; AAC51778.1; -			
DR	HSSP; P19438; INCF.			
DR	INTERPRO; IPR000488; -			
DR	INTERPRO; IPR001368; -			
DR	PFAM; PF00020; TNFR_c6; 2.			
DR	PFAM; PF00531; death; 1.			
DR	PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_2.			
DR	PROSITE; PSS0017; DEATH_DOMAIN; 1.			
DR	PROSITE; PSS0050; TNFR_NGFR_2; 2.			
SO	SEQUENCE 440 AA; 47850 MW; 603005AF2A8B4870 CRC64;			
Query Match	100.0%;	Score 2327;	DB 4;	Length 440;
Best Local Similarity	100.0%;	Pred. No. 1.7e-180;		
Matches 440;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MEORGNAPASGARRKRRGPREARARARPRPKTLVVAVALLVSAESALLRQD	60	
DB	1	MEORGNAPASGARRKRRGPREARARARPRPKTLVVAVALLVSAESALLRQD	60	
QY	61	LAPQARAPOQRKRSPSEGLCPGHHISDGRDCISCKYGQDYSTHWNLLFLCRLCTCD	120	

```

|||||
Db 61 LAPQORAPPOQRSSPSSEGLCPPGHHISEDRDCISCKYGQDYSTHWNDDLFCRLCRCD 120
QY 121 SGEVELSPCTTTNTNTVCOCEEGTFRREDSPEMKCKRTGCGRGVAVKGDCTPMSDIECVH 180
Db 121 SGEVELSPCTTTNTNTVCOCEEGTFRREDSPEMKCKRTGCGRGVAVKGDCTPMSDIECVH 180
QY 181 KESGTRHSGEPAAVEETVTSPTGPASPCSLSGIIGTVAAVLLIYAVFVCKSLMKKV 240
Db 181 KESGTRHSGEPAAVEETVTSPTGPASPCSLSGIIGTVAAVLLIYAVFVCKSLMKKV 240
QY 241 LPTLKIGICSGGGGDPPEVRDSSQRPAGEDVNLNEIVSILQPTQVPEQEMEVOEPAEPTGV 300
Db 241 LPTLKIGICSGGGGDPPEVRDSSQRPAGEDVNLNEIVSILQPTQVPEQEMEVOEPAEPTGV 300
QY 301 NMLSPGSEHLEPAEAERQRRRLVPAWEGDPTETLRQCFFDFAVLVPDSWEPLMRK 360
Db 301 NMLSPGSEHLEPAEAERQRRRLVPAWEGDPTETLRQCFFDFAVLVPDSWEPLMRK 360
QY 361 LGIMDNEIKYAKAEAGHDTLYTMLIKWYKNGTGRDASVHTLLDALETGEBRLAKOKIED 420
Db 361 LGIMDNEIKYAKAEAGHDTLYTMLIKWYKNGTGRDASVHTLLDALETGEBRLAKOKIED 420
QY 421 HLISGKFMYLEGNADSAMS 440
Db 421 HLISGKFMYLEGNADSAMS 440

RESULT 2
ID 015531 PRELIMINARY; PRT; 440 AA.
AC 015531;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DE APOPTOSIS INDUCING PROTEIN.
GN TRICK2B OR DR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Screation G.R., Mongkolkeasapaya J., Xu X., Cowper A.E., McMichael A.J.,
RA Bell A.J.;
RL Curr. Biol. 0:0-0(1997).
RN [2]
RP SEQUENCE FROM N.A.
RA Schneider F., Bodmer J.-L., Thome M., Holler N., Hofmann K.,
RA Tschopp J.;
RL FEBS Lett. 0:0-0(1997).
RN [3]
RP SEQUENCE FROM N.A.
RA Arai T., Akiyama Y., Okabe S., Saito K., Iwai T., Yuasa Y.;
RT "Genomic Structure and Mutation Analyses of the DR5/TRAIL receptor 2
RT Gene in Colorectal Carcinoma."
RT Submitted (MAY-1998) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF018658; AAB70578.1; -
DR EMBL; AF016266; AAB81180.1; -
DR EMBL; AB014718; BAA3723.1; -
DR EMBL; AB014710; BAA3723.1; JOINED.
DR EMBL; AB014712; BAA3723.1; JOINED.
DR EMBL; AB014711; BAA3723.1; JOINED.
DR EMBL; AB014713; BAA3723.1; JOINED.
DR EMBL; AB014714; BAA3723.1; JOINED.
DR EMBL; AB014715; BAA3723.1; JOINED.
DR EMBL; AB014716; BAA3723.1; JOINED.
DR EMBL; AB014717; BAA3723.1; JOINED.
DR HSSP; P19438; INCF.
DR INTERPRO; IPR000488; -
DR INTERPRO; IPR001368; -
DR PFAM; PF00020; TNFR_C6; 2.
DR PFAM; PF00531; death_1.

```

```

DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_2.
DR PROSITE; PS50017; DEATH_DOMAIN_1.
DR PROSITE; PS50050; TNFR_NGFR_2; 2.
SQ SEQUENCE 440 AA; 47894 MM; 7E9367DF3ED24DDE CRC64;

Query Match 99.4%; Score 2313; DB 4; Length 440;
Best Local Similarity 99.5%; Pred. No. 2.3e-179;
Matches 438; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MEORGONAPASGARRKHGPGPREARGARPGPRVPTLVVVAVLLVSASALITQOD 60
Db 1 MEORGONAPASGARRKHGPGPREARGARGLVPTVIVVVAVLLVSASALITQOD 60
QY 61 LAPQORAPPOQRSSPSSEGLCPPGHHI SEDGRDCISCKYGQDYSTHWNDDLFCRLCRCD 120
Db 61 LAPQORAPPOQRSSPSSEGLCPPGHHI SEDGRDCISCKYGQDYSTHWNDDLFCRLCRCD 120
QY 121 SGEVELSPCTTTNTNTVCOCEEGTFRREDSPEMKCKRTGCGRGVAVKGDCTPMSDIECVH 180
Db 121 SGEVELSPCTTTNTNTVCOCEEGTFRREDSPEMKCKRTGCGRGVAVKGDCTPMSDIECVH 180
QY 181 KESGTRHSGEPAAVEETVTSPTGPASPCSLSGIIGTVAAVLLIYAVFVCKSLMKKV 240
Db 181 KESGTRHSGEPAAVEETVTSPTGPASPCSLSGIIGTVAAVLLIYAVFVCKSLMKKV 240
QY 241 LPTLKIGICSGGGGDPPEVRDSSQRPAGEDVNLNEIVSILQPTQVPEQEMEVOEPAEPTGV 300
Db 241 LPTLKIGICSGGGGDPPEVRDSSQRPAGEDVNLNEIVSILQPTQVPEQEMEVOEPAEPTGV 300
QY 301 NMLSPGSEHLEPAEAERQRRRLVPAWEGDPTETLRQCFFDFAVLVPDSWEPLMRK 360
Db 301 NMLSPGSEHLEPAEAERQRRRLVPAWEGDPTETLRQCFFDFAVLVPDSWEPLMRK 360
QY 361 LGIMDNEIKYAKAEAGHDTLYTMLIKWYKNGTGRDASVHTLLDALETGEBRLAKOKIED 420
Db 361 LGIMDNEIKYAKAEAGHDTLYTMLIKWYKNGTGRDASVHTLLDALETGEBRLAKOKIED 420
QY 421 HLISGKFMYLEGNADSAMS 440
Db 421 HLISGKFMYLEGNADSAMS 440

RESULT 3
ID 015508 PRELIMINARY; PRT; 411 AA.
AC 015508;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DE P53-REGULATED DNA DAMAGE-INDUCIBLE CELL DEATH RECEPTOR (FAS-LIKE
DE PROTEIN PRECURSOR).
GN KILLER OR DR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE-OVARIAN;
RA Wu G.S., el-Deiry W.S.;
RL Nat. Genet. 16:0-0(1997).
RN [2]
RP SEQUENCE FROM N.A.
RA MEDLINE=97390508; PubMed=9242610;
RA Pan G., Ni J., Wei Y.F., Yu G., Gentz R., Dixit V.M.;
RT "An antagonist decoy receptor and a death domain-containing receptor
RT for TRAIL."
RL Science 277:815-818(1997).
RN [3]
RP SEQUENCE FROM N.A.
RA Cao X., Zhang W., Wan T.;
RT Submitted (MAY-1999) to the EMBL/Genbank/DBJ databases.

```

DR EMBL: AF022386; AAB71949.1; -
DR EMBL: AF012628; AAB67109.1; -
DR EMBL: AF153687; AAF75587.1; -
DR HSSP: P19438; 1EXT.
DR INTERPRO: IPR000488; -
DR INTERPRO: IPR001368; -
DR PFAM: PF00020; TNR_C6; 2.
DR PFAM: PF00531; death; 1.
DR PROSITE: PS00652; TNR_NGFR_1; UNKNOWN_2.
DR PROSITE: PS50017; DEATH_DOMAIN; 1.
DR PROSITE: PS50050; TNR_NGFR_2; 2.
SO SEQUENCE 411 AA; 45083 MW; 57D5020E72CC954 CRC64;

Query Match 92.5%; Score 2151.5; DB 4; Length 411;
Best Local Similarity 93.4%; Pred. No. 2.5e-166;
Matches 411; Conservative 0; Mismatches 0; Indels 29; Gaps 1;
QY 1 MEORGONAPASGARKRHGPGPREARGARPGPVKTLVVAVALLVSAESALITQOD 60
DB 1 MEORGONAPASGARKRHGPGPREARGARPGPVKTLVVAVALLVSAESALITQOD 60
QY 61 LAQOQRAAPQOKRSSPSEGLCPGHHISEDRGRCISCKYGQDYSTHNDLLFCLRCTCD 120
DB 61 LAQOQRAAPQOKRSSPSEGLCPGHHISEDRGRCISCKYGQDYSTHNDLLFCLRCTCD 120
QY 121 SGEVELSPCTTNTNTVQCCEGTFFREDSPEMCKRCRTGCPGKVKVGDCTPMSDIECVH 180
DB 121 SGEVELSPCTTNTNTVQCCEGTFFREDSPEMCKRCRTGCPGKVKVGDCTPMSDIECVH 180
QY 181 KESGTHSGAPAVEETVTSPTGPASPCSLSGIIGVTAAVLAVALVAVVCKSLMKV 240
DB 181 KE-----SGIIGVTAAVLAVALVAVVCKSLMKV 211
QY 241 LPTLKIGICSGGGDPPEVDRSSORPGAEDNVLYNEIVSILOPTQVPEQEMVQEPAPETGV 300
DB 212 LPTLKIGICSGGGDPPEVDRSSORPGAEDNVLYNEIVSILOPTQVPEQEMVQEPAPETGV 271
QY 301 NMLSPGESEHLEPAAERQORRLVPAPEGDTETLRQCFDFADLVFPDSWEPLMRK 360
DB 272 NMLSPGESEHLEPAAERQORRLVPAPEGDTETLRQCFDFADLVFPDSWEPLMRK 331
QY 361 LGMDNEIKYAKAEAGHRTLYTMLIKVNTKGRDASVHTLLDALETLGERLAKOKIED 420
DB 332 LGMDNEIKYAKAEAGHRTLYTMLIKVNTKGRDASVHTLLDALETLGERLAKOKIED 391
QY 421 HLSSGKFMYLEGNADSAMS 440
DB 392 HLSSGKFMYLEGNADSAMS 411

RESULT 4
ID 014720 PRELIMINARY; PRT; 411 AA.
AC 014720;
DT 01-JAN-1998 (TREMblrel. 05, Created)
DT 01-JAN-1998 (TREMblrel. 05, Last sequence update)
DT 01-MAY-2000 (TREMblrel. 13, Last annotation update)
DE DEATH RECEPTOR 5.
GN DR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97390509; Pubmed=9242611;
RA Sheridan J.P., Marsters S.A., Pitti R.M., Gurney A., Skubatch M.,
RA Baldwin D., Ramakrishnan L., Gray C.L., Baker K., Wood W.I.,
RA Goddard A.D., Godowski P., Ashkenazi A.,
RT "Control of TRAIL-induced apoptosis by a family of signaling and decoy
RT receptors."
RL Science 277:818-821(1997).

DR EMBL: AF012535; AAB67103.1; -
DR HSSP: P19438; 1EXT.
DR INTERPRO: IPR000488; -
DR INTERPRO: IPR001368; -
DR PFAM: PF00020; TNR_C6; 2.
DR PFAM: PF00531; death; 1.
DR PROSITE: PS00652; TNR_NGFR_1; UNKNOWN_2.
DR PROSITE: PS50017; DEATH_DOMAIN; 1.
DR PROSITE: PS50050; TNR_NGFR_2; 2.
SO SEQUENCE 411 AA; 45081 MW; 069BDD63CA08953 CRC64;

Query Match 91.9%; Score 2138.5; DB 4; Length 411;
Best Local Similarity 93.0%; Pred. No. 2.9e-165;
Matches 409; Conservative 1; Mismatches 1; Indels 29; Gaps 1;
QY 1 MEORGONAPASGARKRHGPGPREARGARPGPVKTLVVAVALLVSAESALITQOD 60
DB 1 MEORGONAPASGARKRHGPGPREARGARPGPVKTLVVAVALLVSAESALITQOD 60
QY 61 LAQOQRAAPQOKRSSPSEGLCPGHHISEDRGRCISCKYGQDYSTHNDLLFCLRCTCD 120
DB 61 LAQOQRAAPQOKRSSPSEGLCPGHHISEDRGRCISCKYGQDYSTHNDLLFCLRCTCD 120
QY 121 SGEVELSPCTTNTNTVQCCEGTFFREDSPEMCKRCRTGCPGKVKVGDCTPMSDIECVH 180
DB 121 SGEVELSPCTTNTNTVQCCEGTFFREDSPEMCKRCRTGCPGKVKVGDCTPMSDIECVH 180
QY 181 KESGTHSGAPAVEETVTSPTGPASPCSLSGIIGVTAAVLAVALVAVVCKSLMKV 240
DB 181 KE-----SGIIGVTAAVLAVALVAVVCKSLMKV 211
QY 241 LPTLKIGICSGGGDPPEVDRSSORPGAEDNVLYNEIVSILOPTQVPEQEMVQEPAPETGV 300
DB 212 LPTLKIGICSGGGDPPEVDRSSORPGAEDNVLYNEIVSILOPTQVPEQEMVQEPAPETGV 271
QY 301 NMLSPGESEHLEPAAERQORRLVPAPEGDTETLRQCFDFADLVFPDSWEPLMRK 360
DB 272 NMLSPGESEHLEPAAERQORRLVPAPEGDTETLRQCFDFADLVFPDSWEPLMRK 331
QY 361 LGMDNEIKYAKAEAGHRTLYTMLIKVNTKGRDASVHTLLDALETLGERLAKOKIED 420
DB 332 LGMDNEIKYAKAEAGHRTLYTMLIKVNTKGRDASVHTLLDALETLGERLAKOKIED 391
QY 421 HLSSGKFMYLEGNADSAMS 440
DB 392 HLSSGKFMYLEGNADSAMS 411

RESULT 5
ID 015517 PRELIMINARY; PRT; 411 AA.
AC 015517;
DT 01-JAN-1998 (TREMblrel. 05, Created)
DT 01-JAN-1998 (TREMblrel. 05, Last sequence update)
DT 01-MAY-2000 (TREMblrel. 13, Last annotation update)
DE CYTOTOXIC TRAIL RECEPTOR-2.
GN DR5 OR TRICK2A OR ZTNFR9.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Macfarlane M., Ahmad M., Srinivasula S.M., Fernandes-Alnemri T.,
RA Cohen G.M., Alnemri E.S.,
RL J. Biol. Chem. 0:0-0(1997).
RN [2]
RP SEQUENCE FROM N.A.
RA Sreteron G.R., Mongkolsapaya J., Xu X., Cowper A.E., McMichael A.J.,
RA Bell A.U.,
RL Curr. Biol. 0:0-0(1997).
RN [3]

RP SEQUENCE FROM N.A.
 RX MEDLINE-98090092; PubMed-9430227;
 RA Chaudhary P.M., Eby M., Jasmin A., Bookwalter A., Murray J., Hood L.;
 RT "Death receptor 5, a new member of the TNF family, and DR4 induce
 RT FADD-dependent apoptosis and activate the NF-kappaB pathway."
 RL Immunity 7:821-830(1997).
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Chaudhary P.M., Eby M., Jasmin A., Bookwalter A., Hood L.;
 RA Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RA Fairah T., Vu T., Gilbert T., Gross J., O'Hara P.;
 RT "Homo sapiens homolog of tumor necrosis factor receptor."
 RT Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF020501; AAB7412.1; -;
 DR EMBL: AF018657; AAB70577.1; -;
 DR EMBL: AF016268; AAC01565.1; -;
 DR EMBL: AF192548; AAF07175.1; -;
 DR HSSP: P19438; TEXT.
 DR INTERPRO: IPR000488; -;
 DR INTERPRO: IPR001368; -;
 DR PFAM: PF00020; TNFR_c6; 2.
 DR PFAM: PF00531; death; 1.
 DR PROSITE: PS00652; TNFR_NGFR_1; UNKNOWN_2.
 DR PROSITE: PS50017; DEATH_DOMAIN; 1.
 DR PROSITE: PS50050; TNFR_NGFR_2; 2.
 DR RECEPTOR.
 SQ SEQUENCE 411 AA; 45127 MW; D76ALC9B2FC747F9 CRC64;

Query Match 91.9%; Score 2137.5; DB 4; Length 411;
 Best Local Similarity 93.0%; Pred. No. 3.5e-165;
 Matches 409; Conservative 0; Mismatches 2; Indels 29; Gaps 1;

QY 1 MGRCGNAAASGARRRHPGPREANGARPPVPTLVVAAVLLVSAESALITQOD 60
 DB 1 MGRCGNAAASGARRRHPGPREANGARPPVPTLVVAAVLLVSAESALITQOD 60
 QY 61 LAPQRAAPQOKRSSPSEGLCPGHHIISDGRDCISCKTGODSTHNDLLFCLRTG 120
 DB 61 LAPQRAAPQOKRSSPSEGLCPGHHIISDGRDCISCKTGODSTHNDLLFCLRTG 120
 QY 121 SGEVELSPCTTTRNTVCOCEEGTFREDSPEMCKRCRTGCPGMVVGDCPTMSDIECVH 180
 DB 121 SGEVELSPCTTTRNTVCOCEEGTFREDSPEMCKRCRTGCPGMVVGDCPTMSDIECVH 180
 QY 181 KESGTHSEAEAVETVTSPTGPASPCSLGIIIGTVAAVVLIVAVFVCKSLMKRY 240
 DB 181 KE-----SGIIIGTVAAVVLIVAVFVCKSLMKRY 211
 QY 241 LPYLKIGCGGGGDPPEVRVRSORPGADNVLAIEYSILOPTOVPEQMEVPEAPPTGV 300
 DB 212 LPYLKIGCGGGGDPPEVRVRSORPGADNVLAIEYSILOPTOVPEQMEVPEAPPTGV 271
 QY 301 NMLSPGSESHLLEPAEERSQRRRLVLPANEGDPTETLRQCFDDFADLVPFDSWPELMRK 360
 DB 272 NMLSPGSESHLLEPAEERSQRRRLVLPANEGDPTETLRQCFDDFADLVPFDSWPELMRK 331
 QY 361 LGLMNEIKVAAEAAGHDTLYTMLIKVVKNTGRDASVHTLLDALETIGERLAKOKIED 420
 DB 332 LGLMNEIKVAAEAAGHDTLYTMLIKVVKNTGRDASVHTLLDALETIGERLAKOKIED 391
 QY 421 HLSSGKFMYLEGNADSAMS 440
 DB 392 HLSSGKFMYLEGNADSAMS 411

RESULT 6
 ID 000220 PRELIMINARY; PRT: 468 AA.
 AC 000220;
 DT 01-JUL-1997 (TREMblrel. 04, Created)

DT 01-JUL-1997 (TREMblrel. 04, Last sequence update)
 DT 01-OCT-2000 (TREMblrel. 15, Last annotation update)
 DE CYTOTOXIC LIGAND TRAIL RECEPTOR.
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE-97238921; PubMed-9082980;
 RA Pan G., O'Rourke K., Chinaiyan A.M., Gentz R., Edner R., Ni J.,
 RA Dixit V.M.;
 RT "The receptor for the cytotoxic ligand TRAIL."
 RT Science 276:1111-1133(1997).
 DR EMBL: U90875; AAC51226.1; -;
 DR HSSP: P19438; TEXT.
 DR INTERPRO: IPR000488; -;
 DR INTERPRO: IPR001368; -;
 DR PFAM: PF00020; TNFR_c6; 2.
 DR PFAM: PF00531; death; 1.
 DR PROSITE: PS00652; TNFR_NGFR_1; UNKNOWN_2.
 DR PROSITE: PS50017; DEATH_DOMAIN; 1.
 DR PROSITE: PS50050; TNFR_NGFR_2; 2.
 DR RECEPTOR.
 SQ SEQUENCE 468 AA; 50025 MW; 1E85DCDC2C8760F7 CRC64;

Query Match 45.6%; Score 1061.5; DB 4; Length 468;
 Best Local Similarity 52.0%; Pred. No. 5.8e-78;
 Matches 234; Conservative 41; Mismatches 118; Indels 57; Gaps 8;

QY 5 GONAPASGARRRHPGPREANGARPPVPTLVVAAVLLVSAESALITQODLAP 63
 DB 60 GGHGSGAR-ARRGRAPGRPAEASPRLVHTKTFEVVGVLLQVPPSSANTIKH---- 115
 QY 64 GQRAAPQOKRSSPSEGLCPGHHIISDGRDCISCKTGODSTHNDLLFCLRTGDSGE 123
 DB 116 -OSIGTQWEHSPLELCPGSHRSEBPGACNCTEGVGTNASNNLFCACPCTACKSDE 174
 QY 124 VELSPCTTTRNTVCOCEEGTFREDSPEMCKRCRTGCPGMVVGDCPTMSDIECVHES 183
 DB 175 EERSPCTTTRNTVCOCEEGTFREDSPEMCKRCRTGCPGMVVGDCPTMSDIECVHES 234
 QY 184 GTHSGEAEVAVETVTSPTGPASPCSLGIIIGTVAAVVLIVAVFVCKSLMKRYLPY 243
 DB 235 GNGHN-----IWLIVTVTVPLLVAVL----- 259
 QY 244 LKIGC-----SGGGDPPEVRVRS-----QRPAGEDNVLAIEYSILO--PTOVPEQME 290
 DB 260 ---VCCIGSGGGGDPKCMKDFWRLGLRPGADNAHNEILSNADSLSTFVSEQOME 316
 QY 291 VOEPAPPTGVNMLSPGSESHLLEPAEERSQRRRLVLPANEGDPTETLRQCFDDFADLVP 350
 DB 317 SOEPADLTGVYVQSGEACGLGPAEAGSORRLVLPANAGADPTETLMLEFFDFANIVP 376
 QY 351 FDSWPELMRKIGLMDNEIKVAAEAAGHDTLYTMLIKVVKNTGRDASVHTLLDALETIG 410
 DB 377 FDSWQMLRKOLDLTNEIDIVVAGTAGGDAIYAMLKMKVKTGKNASIRHTLLDALEHME 436
 QY 411 ERLAKOKIEDHLSSGKFMYLEGNADSAMS 440
 DB 437 ERHAREKTIODLLVDSGKPYLEDGTGSAYS 466

RESULT 7
 ID 09UBN6
 AC 09UBN6; PRELIMINARY; PRT: 386 AA.
 DT 01-MAY-2000 (TREMblrel. 13, Created)
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
 DT 01-OCT-2000 (TREMblrel. 15, Last annotation update)
 DE DECOY RECEPTOR 2.
 GN TRAIL-R4.
 OS Homo sapiens (Human).

RESULT 9
ID 0902M4 PRELIMINARY; PRT; 381 AA.
AC 0902M4;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, last sequence update)
DT 01-JUN-2000 (Tremblrel. 14, last annotation update)
DE KILLER/DR5 TRAIL DEATH-INDUCING RECEPTOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN NCBI_TaxID=10090;
[1]
RP SEQUENCE FROM N.A.
RA MEDLINE=99310501; PubMed=10383128;
WU G.S.; Burns T.E.; Zhan Y.; Alnemri E.S.; El-Deiry W.S.;
RT "Molecular cloning and functional analysis of the mouse homologue of
RT the KILLER/DR5 tumor necrosis factor-related apoptosis-inducing ligand
RT (TRAIL) death receptor."
RL Cancer Res. 59:2770-2775(1999).
DR EMBL: AF176833; AAD52656.1; -;
DR INTERPRO: IPR000488; -;
DR INTERPRO: IPR001368; -;
DR PFAM: PF00020; TNR_C6; 2.
DR PFAM: PF00531; death; 1.
DR PROSITE: PS00652; TNR_NGFR.1; UNKNOWN_2.
DR PROSITE: PS50017; DEATH_DOMAIN.1.
DR PROSITE: PS50050; TNR_NGFR_2; 2.
KM Receptor.
SQ SEQUENCE 381 AA; 42164 MW; 22531758F4ADE0A CRC64;

Query Match 25.3%; Score 588; DB 11; Length 381;
Best Local Similarity 34.3%; Pred. No. 1e-39;
Matches 148; Conservative 67; Mismatches 148; Indels 68; Gaps 10;

QY 1 MEORGNAPASGARKRHPGPREARGARPPVPTLVVAAYLVVAALVLSASALITQOD 60
DB 1 MEPPGSTPTASAAARADHYTP---GLRP---LPRRLIYSFALLAVLQAVFVPTANP 53
QY 61 LAPQORAPQOKRSSPSEGLCPPGHHISEGDRDCISCKYGODYSTHMDLL-FCLRCTRC 119
DB 54 PAHNRPAQLQREBESPSRGPCLAGYLSEG--NCKPCREGIDYTSNHSNLSDCITLCTVC 111
QY 120 DSGEVELSPCTTNTNTVQCCGEGTFREEDSPEMCRKCTGCRGMKVGDCPTMSDIECV 179
DB 112 KEDKVVETRCNTTNTVCRCKPGTFEDKDSPEICQSC-SNCTDGEELTSCPTRENKCV 170
QY 180 HKESGTRKSGEAPAVEETVTSPTGSPASCSLSGIIIGVYAAVVLVAAYVFCCKSLMK 239
DB 171 SK-----TAMASWHKLGIMIGLVVYVLLIGALLVWKGMARQ 208
QY 240 VLPYKLGICSGGGGPERVDRSSORPGAEDVNLNEIYSLILOPTVQEGEVEQPAEPTG 299
DB 209 WILCKIRKGE--RDPESA-----NSVHSLIDROTSS----- 238
QY 300 VMLSPGSEHLEPAEARSORRLVLANEGDPTETLRQCFDPAFLVPDPSWEPLMR 359
DB 239 ----TTNDSNHNTEPGKQKT-GKRLVAVNGNDSADDLKTFEYCSDIVPDPSWNRMLR 293
QY 360 KLGLMDNEIKYAKAEAGHRDTLYTMLIKWVKTRGRASVHTLLDALETIGERLAKOKIE 419
DB 294 QUGLNDNOIOWKAEITLYTRREALYOMLKMWHQGRSASINHLIDLALAEVERDAMEKIE 353
QY 420 DHLLSGKFWY 430
DB 354 DYAVKSGRFTY 364

RESULT 10
ID 09JUL6

ID 09JUL6 PRELIMINARY; PRT; 381 AA.
AC 09JUL6;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, last sequence update)
DT 01-OCT-2000 (Tremblrel. 15, last annotation update)
DE TRAIL RECEPTOR KILLER/DR5 HOMOLOGUE.
GN MK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN NCBI_TaxID=10090;
[1]
RP SEQUENCE FROM N.A.
RA TISSUE=SPLEEN.
RC Nakamura Y.; Tamari M.; Watanabe O.;
RT "Mouse TRAIL receptor."
RL Submitted (Aug-1999) to the EMBL/Genbank/DBJ databases.
DR EMBL: AB031081; BAA06462.1; -;
KM Receptor.
SQ SEQUENCE 381 AA; 42223 MW; 2F7999EA2EB485B1 CRC64;

Query Match 24.9%; Score 580; DB 11; Length 381;
Best Local Similarity 33.9%; Pred. No. 4.5e-39;
Matches 146; Conservative 69; Mismatches 148; Indels 68; Gaps 11;

QY 1 MEORGNAPASGARKRHPGPREARGARPPVPTLVVAAYLVVAALVLSASALITQOD 60
DB 1 MEPPGSTPTASAAARADHYTP---GLRP---LRLIYSFALLAVLQAVFVPTANP 54
QY 61 LAPQORAPQOKRSSPSEGLCPPGHHISEGDRDCISCKYGODYSTHMDLL-FCLRCTRC 119
DB 55 -AHNRPAQLQREBESPSRGPCLAGYLSEG--NCKPCREGIDYTSNHSNLSDCITLCTVC 111
QY 120 DSGEVELSPCTTNTNTVQCCGEGTFREEDSPEMCRKCTGCRGMKVGDCPTMSDIECV 179
DB 112 KEDKVVETRCNTTNTVCRCKPGTFEDKDSPEICQSC-SNCTDGEELTSCPTRENKCV 170
QY 180 HKESGTRKSGEAPAVEETVTSPTGSPASCSLSGIIIGVYAAVVLVAAYVFCCKSLMK 239
DB 171 SK-----TAMASWHKLGIMIGLVVYVLLIGALLVWKGMARQ 208
QY 240 VLPYKLGICSGGGGPERVDRSSORPGAEDVNLNEIYSLILOPTVQEGEVEQPAEPTG 299
DB 209 WILCKIRKGE--RDPESA-----NSVHSLIDROTSS----- 238
QY 300 VMLSPGSEHLEPAEARSORRLVLANEGDPTETLRQCFDPAFLVPDPSWEPLMR 359
DB 239 ----TTNDSNHNTEPGKQKT-GKRLVAVNGNDSADDLKTFEYCSDIVPDPSWNRMLR 293
QY 360 KLGLMDNEIKYAKAEAGHRDTLYTMLIKWVKTRGRASVHTLLDALETIGERLAKOKIE 419
DB 294 QUGLNDNOIOWKAEITLYTRREALYOMLKMWHQGRSASINHLIDLALAEVERDAMEKIE 353
QY 420 DHLLSGKFWY 430
DB 354 DYAVKSGRFTY 364

RESULT 11
ID 09JUL5 PRELIMINARY; PRT; 385 AA.
AC 09JUL5;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, last sequence update)
DT 01-OCT-2000 (Tremblrel. 15, last annotation update)
DE TRAIL RECEPTOR2 KILLER/DR5 HOMOLOGUE.
GN MK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN NCBI_TaxID=10090;
[1]

RP SEQUENCE FROM N.A.
 RA Nakamura Y., Tamari M., Watanabe O.;
 RT "Mouse TRAIL receptor genomic."
 RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AB031082; BAA96463.1; -;
 KW Receptor.
 SQ SEQUENCE 385 AA; 42676 MW; 4FD089FCDA134159 CRC64;

Query Match 24.3%; Score 565; DB 11; Length 385;
 Best Local Similarity 33.0%; Pred. No. 7.5e-38;
 Matches 143; Conservative 73; Mismatches 149; Indels 68; Gaps 12;

QY 1 MEORGQAPAPGAKRKRGPRGARGARPGPKTLVVAALLVVAESALITQOD 60
 DB 1 MERRGPSTPASAARADHTP-----GLRPLK--RRLYSFALLMLAMLAIVPVTANP 54
 QY 61 LAPQRAAPQOKRSSPSEGLCPGHHISEDRDCISCKYGQDYSTHWNLL-FCLCRTGC 119
 DB 55 -AHRPAGLQRPESPSPRGCLAGQYLSEG--NCKPCREGIDYTSRSHSLDSCILCTVC 111
 QY 120 DSGEVELSPCTTRNTYCOCEEGTFREDSPEMCRKRTGCPRGMYKVGDCITPMSDIECV 179
 DB 112 KEDVETRNITNTNTECRCKPGTFEDKDSPEICQSC-SNCTDGEELTSCPRENRCYV 170
 QY 180 HKES-GTHSGEAPAVEETVTSPPGPASPCSLGIITGVAAVLIIV-AVEYCKSLW 237
 DB 171 SKRAMASMH-----LGLMIGATLVPPVLLIGALLVMKIGAW 207
 QY 238 KVALPYLKIGSGGGGDPERVDSSORPGAEDVNLVNIISLOTPQVEQEMEVOEPAEP 297
 DB 208 ROWMLCIKRAYPCGERPESA-----NSVHLSLDRQTS----- 242
 QY 298 TGVNMLSPGSEHLEPAEAEBSORRLVLANEGDPTFLRCDFADALVPRDSWEPL 357
 DB 243 -----TTNDSNHTGEGKQKT-GKKLLVNVGNDASADLKEFECSIVIPDSVNR 295
 QY 358 MRKGLDNEIKYAKAEAGHRTLYTMLIKVWKTGRDASVHTLDALTEGLERLAKOK 417
 DB 296 MROGLTDNIOVRAETLYTRALYQMLLKWHRQGRSASINHLDALEAVEERDAMEK 355
 QY 418 IEDHLSSGKFWY 430
 DB 356 IEDYAVKSGRFTY 368
 RESULT 12
 ID 057408 PRELIMINARY; PRT; 368 AA.
 AC 057408;
 DT 01-JUN-1998 (Tremblrel. 06, Created)
 DT 01-OCT-1998 (Tremblrel. 06, Last sequence update)
 DT 01-OCT-2000 (Tremblrel. 15, Last annotation update)
 DE SUBGROUP E ALV RECEPTOR.
 OS Meleagris gallinapavo (Common turkey).
 OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Meleagrididae; Meleagris.
 NC NCBL_TaxID=9103;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Adkins H.B., Brojatsch J., Naughton J., Rolis M.M., Pesola J.M.,
 RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF006002; AAB93987.1; -;
 DR HSSP: P19438; 1EXT
 DR INTERPRO: IPR000486; -;
 DR INTERPRO: IPR001368; -;
 DR INTERPRO: IPR001450; -;
 DR INTERPRO: IPR001865; -;
 DR PRAM: PF00020; TNR_6; 2.
 DR PRAM: PF00531; death; 1.
 DR PROSITE: PS00198; 4FEAS_PRREROXIN; UNKNOWN_1.
 DR PROSITE: PS00652; TNR_NGFR_1; UNKNOWN_2.

DR PROSITE: PS00962; RIBOSOMAL_S2_1; UNKNOWN_1.
 DR PROSITE: PS50017; DEATH_DOMAIN; 1.
 DR PROSITE: PS50050; TNR_NGFR_2; 2.
 SQ SEQUENCE 368 AA; 41020 MW; 5701AC2A6DAF87E2 CRC64;

Query Match 21.0%; Score 488.5; DB 13; Length 368;
 Best Local Similarity 32.1%; Pred. No. 1.1e-31;
 Matches 132; Conservative 53; Mismatches 163; Indels 63; Gaps 11;

QY 36 KTLVVAVALVLSASALITQODLAPQORAPQOKRSSPSEL-----CPRHNI 87
 DB 2 RSALRCPVLLLLAVVHL-----GSAAVKRAVSDVLRKDPYSKKCPMCTYL 52
 QY 88 SEDRDCISCKYGQDYSTHWNLLFCLCRTCRDSEGEVELSPCTTRNTYCOCEGTFREE 147
 DB 53 ANDSRCLPCK-KDEYEYRNDPFCGLGCTCRDQVEVSPCNSTRITRACKNGTCLP 111
 QY 148 DSP-EMCRKRTGCPRGMYKVGDCITPMSDIECVHKESGTHSGEAPAVEETVTSPPGTPA 206
 DB 112 DHPCEMCKQTCRCPKQVRIACTQSDLR-----GPIDNS 150
 QY 207 SPCLSGIITGVAAVVAVVAVFCVCKSLMKKYLPLKIGCSGGGDPERVDSS----- 262
 DB 151 SFTTGTIIISTVLPVVLVFLVLLVLCCLCC-----CRRYSAGSGGVLSSRKPAAVYKIL 202
 QY 263 -ORPGAEDVNLVNIISLOTPQVEQEMEVOEPAE--PTGVNMLSPGSEHLEPAEAE 319
 DB 203 LQRMGIDNNCNE--QIYQOQOQOQOQLITTEQSEVPRGEV-----EVEVAPRTNVE 256
 QY 320 SORRRLVLANEGDPTFLRCDFADLVFPDSWEPLMRKGLMDNEIKYAKAEAGHR 379
 DB 257 TQNR--LVVPKQDPLVLSSEFNTFVDLVFPQWRFRGALGIRENNLVQAQENDRESG 314
 QY 380 DTLVTLIKVWKTGRDASVHTLDALTEGLERLAKKIEDHLSSGKFWY 430
 DB 315 EPLYQMLIMLNKESKASVNTLETLSQISLGVADIASSLRNGYFOY 365
 RESULT 13
 ID 091AR7 PRELIMINARY; PRT; 368 AA.
 AC 091AR7;
 DT 01-OCT-2000 (Tremblrel. 15, Created)
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
 DT 01-OCT-2000 (Tremblrel. 15, Last annotation update)
 DE TVBS1.
 GN Gallus gallus (Chicken).
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 NC NCBL_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Adkins H.B., Brojatsch J., Young J.A.T.;
 RT "Identification and Characterization of a TNR-Related Receptor for
 RT Subgroups B/D/E Avian Leukosis Viruses Reveals Cysteine Residues
 RT Required Specifically for Subgroup B Virus Entry";
 RL J. Virol. 74:3572-3578(2000).
 DR EMBL: AF161713; AAF60221.1; -;
 SQ SEQUENCE 368 AA; 41531 MW; 0553CE531DEBA7C6 CRC64;

Query Match 20.4%; Score 474.5; DB 13; Length 368;
 Best Local Similarity 33.0%; Pred. No. 1.5e-30;
 Matches 137; Conservative 50; Mismatches 157; Indels 71; Gaps 14;

QY 36 KTLVVAVALVLSASALITQODLAPQORAPQOKRSSPSE-----GLCPGHHI 87
 DB 2 RSALRCLCPVLLLLFAVQL-----GSAAVKRRARSDQKRDILRRKCPMCTYE 52
 QY 88 SEDRDCISCKYGQDYSTHWNLLFCLCRTCRDSEGEVELSPCTTRNTYCOCEGTFREE 147

```

Db      53 ANDSIQCLPCK-KDEYTEYPNDPKKICGCTCHCEDQVEVSPCIPTRTQCACXNGTFCILP 111
      148 DSP-EMCRKCRGTCGPRGMVAVGDCPTWMSDIECHKSGSTGHSEAPAVEETVTSISGTPA 206
      112 DHCECMQCKQTCPECPGVNLAPCTQHSIDL------GPLE- -ISSSSST- 155
      207 SPSCSGIITGVTAAVVLLVAVFVCKSLMKFKVLYLNGKCS- -GGGGDEPR- - 257
      156 - - - - -LMIITFTVLLAVILGLV- - -FWKR- - - - -CSSRHGAGDDDELMSKPS 198
      258 - - -VDRSSQRPAGADNVLNEIVSLIPTQVPEQMEVQEPAPFPQVNMVLSGSEHLLPEA 315
      199 AVVNRLLQRLQIGIDNRCNE- -QIYQNOQOQELIFTAQSSEVPHGVM- -EGTERRTPD- 253
      316 EMERSQRRLLVAVANSGDPTETLRQCFDDPADIVPPDSMEPLMRKICIMDNELKAKAAEA 375
      254 - - -KVTQRKLVAVLGENPAILHRSFNFTVDVPPPEMKRFGRAILDQENDLYLAQHD 310
      376 AGHRDLYMLTIKWNKGTGRDASVHTLLDALETLGERLAKOKIEDHLLSSGKPMY 430
      311 RVSCEFPYQMLNWTWLNQGSKASVNTLLETLPRIIGLSVADIIASFLISKGYQY 365

```

RESULT 14

```

ID      014798      PRELIMINARY:      PRT:      299 AA.
AC      014798:
DT      01-JAN-1998 (TREMBLrel. 05, Created)
DT      01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT      01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE      CYTOTOXIC TRAIL RECEPTOR-3 (LYMPHOCYTE INHIBITOR OF TRAIL) (ANTAGONIST
DE      DECOY RECEPTOR FOR TRAIL/APO-2L).
GN      TRAIL-R3 OR LIT OR TRID OR DCRL.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      MacFarlane M., Ahmad M., Stinivasula S.M., Fernandes-Alnemri T.,
RA      Cohen G.M., Alnemri E.S.,
RA      J. Biol. Chem. 0:0-0(1997).
RN      [2]
RP      SEQUENCE FROM N.A.
RA      Degli-Esposti M.A., Smolak P.J., Walczak H., Naughton J., Huang C.P.,
RA      Dubose R.F., Goodwin R.G., Smith C.A.,
RA      "Cloning and characterization of TRAIL-R3, a novel member of the
RA      emerging TRAIL receptor family."
RA      J. Exp. Med. 186:1165-1170(1997).
RN      [3]
RP      SEQUENCE OF 41-299 FROM N.A.
RA      Mongkolsapaya J., Cowper A., Xu X., Morris G., McMichael A.J.,
RA      Bell J.I., Screaton G.R.,
RA      J. Immunol. 0:0-0(1997).
RN      [4]
RP      SEQUENCE OF 41-299 FROM N.A.
RA      MEDLINE=97390508; PubMed=9242610;
RA      Pan G., Ni J., Wei Y.F., Yu G., Gentz R., Dixit V.M.,
RA      "An antagonist decoy receptor and a death domain-containing receptor
RA      for TRAIL."
RA      Science 277:815-818(1997).
RN      [5]
RP      SEQUENCE OF 41-299 FROM N.A.
RA      MEDLINE=97390509; PubMed=9242611;
RA      Sheridan J.P., Marsters S.A., Pitti R.M., Gurney A., Skubatch M.,
RA      Baldwin D., Ramakrishnan L., Gray C.L., Baker K., Wood W.I.,
RA      Goddard A.D., Godowski P., Ashkenazi A.,
RA      "Control of TRAIL-induced apoptosis by a family of signaling and decoy
RA      receptors."
RA      Science 277:818-821(1997).
DR      EMBL; AF020502; AAB71413.1; -

```

```

DR      EMBL; AF014794; AAC05593.1; -
DR      EMBL; AF033854; AAB87506.1; -
DR      EMBL; AF012629; AAB67110.1; -
DR      EMBL; AF012536; AAB67104.1; -
DR      HSSP; P19438; 1EXT.
DR      INTERPRO; IPR001368; -
DR      PFAM; PF00020; TNFR_c6; 2.
DR      PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_2.
DR      PROSITE; PS00500; TNFR_NGFR_2; 2.
KW      Receptor.
SQ      SEQUENCE      299 AA: 31759 MW; 2435106F847FE1AB CRC64;

```

```

Query Match      20.1%; Score 467; DB 4; Length 299;
Best Local Similarity 39.2%; Pred. No. 4,7e-30;
Matches 112; Conservative 25; Mismatches 87; Indels 62; Gaps 4;

```

```

QY      5 GONAPASAGARRKHGPGPREARGARPPVPTL-VLVAAVLLVSAESALITQODLA 62
      15 GDRAPRPDGRGVRPRRTQDGVGNHTMARIPKTLFVVVYVAVLLPLAYSATFARAEV 74
QY      63 PQRAAPQCKRSPSGCLCPPGHHISEGDRDCISCKYGDYSTHNDLFLCRLCRCSG 122
      75 PQOTVAPQOQRHSFSGECPAGSHRSEHTGACNPCTEGVDYTNASNNESPSCPCTVCKSD 134
QY      123 EVELSPCTTTRNTVCCCEGTFRFEDSPPMCRKCRCTGCPRGVKKYGDCTPMSDIECVH- 180
      135 QKHSSCTITRDTVCCQCKGTFRNENSPMCKKC-SRCPGSEVOVSNGTSMWIDICVEEF 193
QY      181 -----KESG 184
DB      194 GANATVETPAAEETMNTSPGTAPAAEETMNTSPGTAPAAEETMTSPGTAPAAEETM 253
      185 TKHSG-EAPAVEETVTSRGTASPCSLGIIITGVTAAVVLIYAV 229
QY      254 TTSPTGPAPAAEETMTSPGTAPASSHYLSCTIVGIIIVLILIVP 299

```

RESULT 15

```

ID      09PW79      PRELIMINARY:      PRT:      368 AA.
AC      09PW79:
DT      01-MAY-2000 (TREMBLrel. 13, Created)
DT      01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT      01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE      TVB3.
GN      TVB.
OS      Gallus gallus (Chicken).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC      Gallus.
OX      NCBI_TaxID=9031;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      MEDLINE=97100985; PubMed=8945512;
RA      Brojatsch J., Naughton J., Rolis M.M., Zingler K., Young J.A.,
RA      "CARL, a TNFR-related protein, is a cellular receptor for cytopathic
RA      avian leukosis-sarcoma viruses and mediates apoptosis."
RA      Cell 87:845-855(1996).
RN      [2]
RP      SEQUENCE FROM N.A.
RA      Brojatsch J., Naughton J., Young J.A.,
RA      Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
RA      EMBL; AF161712; AAD47256.1; -
DR      HSSP; P19438; 1TNR.
DR      INTERPRO; IPR000488; -
DR      INTERPRO; IPR001368; -
DR      INTERPRO; IPR001450; -
DR      PFAM; PF00020; TNFR_c6; 2.
DR      PFAM; PF00531; death_1.
DR      PROSITE; PS00198; 4FE4S_FERREDOXIN; UNKNOWN_1.
DR      PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR      PROSITE; PS50017; DEATH_DOMAIN; 1.

```


DR PROSITE; PS50050; TNFR_NGFR_2; 2.
SQ SEQUENCE 368 AA; 41515 MW; F558C225AB3750BB CRC64;

Query Match 20.0%; Score 464.5; DB 13; Length 368;

Best Local Similarity 32.8%; Pred. No. 9.7e-30;

Matches 136; Conservative 50; Mismatches 158; Indels 71; Gaps 14;

```
QY 36 KTLVLVAALVLAASALITQODLAPQORAPPOKRSSPSE-----GLCPGCHI 87
DB 2 RSAALRLCPVLLLFPAVOL-----GSAALVKKRADSDLOKPDLYRRKCPMGTYE 52
QY 88 SEDGRDCISCKYGQDYSTHWNLLFCLRCTRCDSGEVELSPCTTNTNTVCQCEGTFREE 147
DB 53 ANDSIQCLPSK-KDEYTEYNDFPKCLGCRTECDQVEVSPCIPTNTQCACKNGTFCLP 111
QY 148 DSP-EMCRKCRCTGCPRGAMVVGDCPTMSDIECVHKEGSKHSGEAPAVETVTSPTPA 206
DB 112 DHPCEMCKQCKQTECPKGOVRLAPCTOHSDLG-----GPLE--ISSSST-- 155
QY 207 SPCSLSGIITGVAAVLAIVAVFVCKSLMKVLPYLKIGCS---GGGDPER----- 257
DB 156 -----LMIITTFVLAIVILGLVY----FWKR-----CSSRHGAGDDDELSTKPS 198
QY 258 --VDRSSQRPAGADNYLNEIVSILOPTQVPEQEMEVQEPAPETGVNMLSPGESEHLLPEA 315
DB 199 AVVNRLLQRLGIQDNRCNE--QIYQNOQOQELLFTAGSEVPHGVEM--EGTERRTDP- 253
QY 316 EARSQRRRLVLANEGDPTETLRQCFDDPADLYFPDSEPLMRKGLGIMDNEIKVAKAEA 375
DB 254 --KVEIQRLVPLVGENPTALHRSFNTPVDVPPPEMKRFGRAIDLQENDLYLAEQHD 310
QY 376 AGHRDTLYTLIKWVNTGRDASVHTLLDALETLGERLAKQIEDHLLSSGKFMY 430
DB 311 RVSCPEPYQMLNTWLNQGSKASVNTLETLPRIGLSGVADITASELISKGYQY 365
```

Search completed: May 23, 2001, 14:20:19
Job time: 89 sec

This Page Blank (uspto)